

FIGURE 1

1 CCCACGCGTCCGGTCCGGAGCTAGAGCTCCAAGGACCCACGCTGTGTCTCTGTGACAGA
61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTCCCCAGT
121 CCAGAAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
241 TGAGAGAGTCTTGGGTGTCTTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG
361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA
421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCTCTGTCCAAGGC
481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
541 TTCCCGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTC
601 TCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
721 AAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCTTGAGGGGCCCTTCTCATCCGGGAG
781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTCACTCCGCCTCAGCCGCCCTGCATCCTGG
841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
901 CGCCTCACCTTCCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC
961 ATCTGTCTGCTACTCAAGGAGCCCTGTGTCTTGCAAGGGCTGGCCCGCTCCCTGGCAAG
1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
1201 GCCCAAAGGAGAGGGCCAAAAGGGAAACCAAGGCTGCACACCTAGAACCCCAATTACGCCT
1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
1321 ATCTAGGGTCCCACCTGTACCCTTGCTCTTTCTCTCTTAGCCCTTAGAAGTCACCTACT
1381 TCCTTCCAGTGCCATGATCCACCTGCGACCTCTAGTGCGAGTGACAGAGAAGGTGGGACC
1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT
1681 GGCTTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGATGG
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCCTCAA
1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTCTTTTTTTTGGAGACGGAGTCTT
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTACCACATTGGCC
2041 AGGCTGGTGTGGAACCTCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCAATTTTGTG
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
2341 CTTTGATTTCCTTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
2401 AGGGAGAGGAAGAAAGAGGGATGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTT
2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA
2521 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 2

1																			M	G
3	S	L	P	S	R	R	K	S	L	P	S	P	S	L	S	S	S	V	Q	G
23	Q	G	P	V	T	M	E	A	E	R	S	K	A	T	A	V	A	L	G	S
43	F	P	A	G	G	P	A	E	L	S	L	R	L	G	E	P	L	T	I	V
63	S	E	D	G	D	W	W	T	V	L	S	E	V	S	E	R	E	L	N	E
83	P	S	V	H	V	A	K	V	S	H	G	W	L	Y	E	G	L	S	R	I
103	K	A	E	E	L	L	L	L	P	G	N	P	G	G	A	F	L	I	R	E
123	S	Q	T	R	R	G	S	Y	S	L	S	V	R	L	S	R	P	A	S	W
143	D	R	I	R	H	Y	R	I	H	C	L	D	N	G	W	L	Y	I	S	P
163	R	L	T	F	P	S	L	Q	A	L	V	D	H	Y	S	E	L	A	D	D
183	I	C	C	L	L	K	E	P	C	V	L	Q	R	A	G	P	L	P	G	K
203	D	I	P	L	P	V	T	V	Q	R	T	P	L	N	W	K	E	L	D	S
223	S	L	L	F	S	E	A	A	T	G	E	E	S	L	L	S	E	G	L	R
243	E	S	L	S	F	Y	I	S	L	N	D	E	A	V	S	L	D	D	A	*

FIGURE 3A

1 CCCACGCGTCCGGTCCGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
121 CCAGAAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
241 TGAGAGAGTTCTGGGTGTCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCAAGCCTTTG
361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCCTGCTGAGGAACAATGGGA
1 M G
421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCCCTCTGTCCAAGGC
3 S L P S R R K S L P S P S L S S S V Q G
481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
23 Q G P V T M E A E R S K A T A V A L G S
541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTGCTGAGACTCGGGGAGCCATTGACCATCGTC
43 F P A G G P A E L S L R L G E P L T I V
601 TCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
63 S E D G D W W T V L S E V S G R E Y N I
661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
83 P S V H V A K V S H G W L Y E G L S R E
721 AAAGCAGAGGAACTGCTGTTGTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAG
103 K A E E L L L L P G N P G G A F L I R E
781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGG
123 S Q T R R G S Y S L S V R L S R P A S W
841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
143 D R I R H Y R I H C L D N G W L Y I S P
901 CGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC
163 R L T F P S L Q A L V D H Y S E L A D D
961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTGTCAGAGGGCTGGCCCGCTCCCTGGCAAG
183 I C C L L K E P C V L Q R A G P L P G K
1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
203 D I P L P V T V Q R T P L N W K E L D S
1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
223 S L L F S E A A T G E E S L L S E G L R
1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
243 E S L S F Y I S L N D E A V S L D D A *
1201 GCCCAAAGGAGAGGCCAAAAGGGAAACCAAGCTGCACACCTAGAACCCCAATTCAGCCT
1261 CCTGGGCACCCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
1321 ATCTAGGGTCCCACCTGTACCCTTGCTCTTTCTCTCTTAGCCCTTAGAAGTCACCTACT
1381 TCCTTCCAGTGCCATGATCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC
1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
1561 ACCATTAACCAGGCCCCACCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIGURE 3B

1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCCCTCAA
1801 ATGTCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTTTTGAGACGGAGTCTT
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTCACCACATTGGCC
2041 AGGCTGGTGTGGAACCTCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTAFTTCATTTTGTG
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
2341 CCTTGATTTCCCTGCTGCCGCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTC
2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA
2522 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAA

1681
1741
1801
1861
1921
1981
2041
2101
2161
2221
2281
2341
2401
2461
2522

FIGURE 4

Homology	Amino acid level	
	Similarity	Identity
human SLAP x mouse SLAP	89.9%	88.0%
human SLAP x human SLAP-2	58.4%	47.4%
mouse SLAP x human SLAP-2	70.0%	58.1%

FIGURE 5

hSLAP-2 1 MGS LPSRRKSLPSPSLSSSVQGGPVTMEAERSKATAVALGSFPAGGPAE
 : . |||. : |. | :|. .
hSLAP 1 . . .MGNSMKSTPAPAERLPNPEGLSDSDFLAVLSDYPSPDISP

51 LSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLS
 | | | : : | | : | . | | | | : | | : | | | : | | |
41 PIFRRGEKLRVISDEGGWKAISLSTGRESYIPGICVARVYHGWLFEGLG

101 REKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRI RHYRI
 | : | | | | | | | | | . | : | | | | : : | | | | | . : : | | | |
91 RDKAEELLQLPDTKVGSMIRESETKKGFYSLSVRHRQVKHYRI

151 HCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCVLQ RAGPLP
 | | | | | | | | | | : | | . | | | | . | | : | | . | | . |
135 FRLPNNWYYISPRLTFQCLDLVNHYSEVADGLCCVLTTPCLTQSTAAPA

201 GKDIPLPVTVQRTPLNWK . . .ELDSSLLFSEAATG.EESLLSEGLRESLS
 : | | | . . . | : | | . | | : | | | | | | | : .
185 VRASSSPVTLRQKTVDWRRVSR LQEDPEGTENPLGVDES LFSYGLRESIA

247 FYISLNDEAVSLDDA
 | : | | | . |
235 SYLSLTSEDNTSFD RKKKSISLMYGGSKRKSSFFSSPPYFED

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

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hSLAP 1  MGNSMKSTPAPAERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRERGEKLR
          . . . . . : . . . . .
mSLAP 1  MGNSMKSTSPPSERPLSSSEGLESDFLAVLTDYPSPDISPPIFRERGEKLR
          . . . . . : . . . . .

          51  VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLRDKAEEELLQL
          . . . . . : . . . . .
          51  VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLRDKAEEELLQL

          101  PDTKVGSGFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF
          . . . . . : . . . . .
          101  PDTKIGSGFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF

          151  QCLEDLVNHYSEVADGLCCVLTTTPCLTQSTAAPAVRAS.....SSPVTLR
          . . . . . : . . . . .
          151  QCLEDLVTHYSEVADGLCCVLTTPCAQNIPAPTSHPSPTSPGSPVTLR

          196  QKTVDWRRVSRLQEDPEGTENPLGVDESLSFSYGLRESIASYLSLTSEDNT
          . . . . . : . . . . .
          201  QKTFDWKRVSRLQEGSEGAENPLRVDESLSFSYGLRESIASYLSLTGDDSS

          246  SFDRKKKKSISLMYGGSKRKSSFFSSPPYFED 276
          . . . . . : . . . . .
          251  SFDRKKKKSLSLMTGSKRKSSFFSAPQYFED 281

```

FIGURE 7

hSLAP-2 1 MG.SLPSRRKSLPS..PSLSSSVQGQGPVTMEAERSKATAVALGSFPAGG
 || |: | | || | ||| :| :| | || | :|.

mSLAP 1 MGNSMKs..TSPPSERP.LSSS...EG...LE...SDFLAV.LTDYPS..

 48 PAELS...LRLGEPLTIVSEDGDWWTVLSEVS.GRE.YNIPSVHVAKVSH

 | :| | | | :| :| | | :| | | | :| :| |

 36 P.DISPPIFRRGEKLRVISDEGGWWKAIS.LSTGRESY.IPGICVARVYH

 93 GWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASW

 ||| :|| | :| |||| | | |. | :| ||| :| :| | |||| |

 83 GWLFEGLGRDKAEELLQLPDTKIGSFMIRESETKKGFYLSVR.HR....

 143 DRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCV

 . :| ||| | | | ||||| | :| | ||||. | | :| | | |

 128 .QVKHYRIFRLPNNWYYISPRLTFQCLEDLVTHYSEVADGLCCVLTTPCL

 193 LQR..A.....GPL..PGKDIPLPVTV.QRTPLNWKELDSSLLFSEAATG

 | | | | | | | | | | | | | | | | | | | | |

 177 AQNIPAPTSHPSPECTSPGS....PVTLRQKT.FDWKRV.SRL..QEGSEG

 233 .E.....ESLLSEGLRESLSFYISL.NDEAVSLD

 | | | | | | | | | | | | | | | | | | | |

 219 AENPLRVDESLFSYGLRESIASYLSLTGDDSSSFD

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 8

